METHODS FOR IDENTIFYING CANCER RISK

ABSTRACT

The present invention provides methods and kits for identifying an increased risk of developing cancer in a subject. The methods include analyzing a first biological sample, such as a blood sample, from the subject for loss of imprinting of the IGF2 gene. According to the methods a loss of imprinting is indicative of an increased risk of developing cancer. The method can include analyzing genomic DNA from the sample for altered methylation of the IGF2 or the H19 gene. The altered methylation for example includes hypomethylation of a differentially methylated region of IGF2, corresponding to SEQ ID NO:1 and/or a polymorphism or fragment thereof, or hypomethylation of a differentially methylated region of H19 corresponding to SEQ ID NO:6, or a polymorphism, or fragment thereof. In certain aspects, hypomethylation of the H19 DMR or the IGF2 DMR indicates an increased risk of developing colorectal cancer.